



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
SEX IDENTIFICATION IN BIRDS

(iii) NUMBER OF SEQUENCES: 41

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/GB96/01341
(B) FILING DATE: 05-JUN-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511439.3
(B) FILING DATE: 06-JUN-1995

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(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

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TECH CENTER 1600/2800

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGTCGGA GGTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC	60
AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTC CAGCCTTAAT	120
AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTGA GCGAAGTTG TTTGGGGATT	180
TTAGTTGGT TTCCCTGTCA CTGTTTCTT TCCTTGAAAC TGACTTCAT TTGCAACATG	240
AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA	300
CATTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTGAG	360
ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC	420
ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA	480
TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG	540
ATGACAGTGG TACAGGAGCT CTGAATTCTT TAGATAAACT ATGAGAGTGG AAACAGAAAT	600
CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTCAA GACTACATTA	660
GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC	720
GGG	723

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAC AGTTACAGAC CAAAAAACCA	60
--	----

CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120
GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG 153

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC 60
CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA ATTACTGAA TAAAGACCTT 120
GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC 60
CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA ATTACTGAA TAAAGACCTT 120
GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60
CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120
GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1 5 10 15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys
20 25 30
Arg Glu Ala Gln Arg Leu Cys Gly Ala
35 40

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1 5 10 15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
20 25 30
Lys Glu Ala Gln Arg Leu Ala Gly Ala
35 40

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1 5 10 15

Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
20 25 30

Lys Glu Ala Gln Arg Leu Ala Gly Ala
35 40

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1 5 10 15

Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
20 25 30

Lys Glu Val Gln Arg Leu Thr Gly Ala
35 40

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC	60
CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG	120
CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAAG AAAGGGGATT CTTGACCTAC	180
ACCTTGTAAC CTGAGTGGAC TTTCTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA	240
GTGATGAAGA AAGTGTAAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG	300
GGTCAGCTTC AGGTTCTGGA TCTGGTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA	360
GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG	420
AGTCTGACAC ATCTAGAGAG AAGAAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT	480
CTGAGTTTG GAAGTCCAGT CCAAGCATAAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA	540
AGCAACAGCA ACAGCAAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA	600
GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG	660
AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG	720
CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAACA	780
AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG	840
GACAGAAGAA GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG	900
ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA	960
CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCAGACTGAAG	1020
AAGATGAATT TGAAACTATA GAGAAGTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA	1080
CTGGTGCCTC AACCAACCATC TATGCCGTTAG AGGCAGATGG TGACCCAAAT GCTGGTTTG	1140
AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA	1200
TCCATAACAC TTGGGAAACT GAAGAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA	1260
AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC	1320
CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT	1380
ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG	1440
ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGAA GATGGTGCTC	1500

TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
CTACTCCCTT	TAAGGACTGC	AAGGTTCTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
TGGGTCTGGG	TAAAACAATA	CAAACAATTT	CTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
AACTGTATGG	CCCTTTCTT	CTGCGCGTGC	CACTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTA	CTTAGGAGAT	ATAACTAGTA	1920
GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTAACAA	1980
TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCCTTGGT	GGTCTCAATT	2040
GGGCATTCCAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
ATCCCTCAA	AGAGCTGTGG	TCTTGTGTC	ATTCATCAT	GCCAGAAAAA	TTTCCTCCT	2220
GGGAAGATTT	TGAAGAGGAG	CATGGCAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
AAGAGCTTGA	ACCATTTTA	CTAAGAAGAG	TTAAAAAAGA	TGTAGAAAAG	TCTTACCTG	2340
CTAAGGTTGA	ACAAATTCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
GGATTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTT	AAAAGGCAGT	ACCTCAGGCT	2460
TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520
CAGATGATAA	TGAATTCTAT	AATAAACAGG	AGGCCTTACA	GCATTTGATA	CGTAGCAGCG	2580
GGAAACTAAT	CCTCTTGAC	AAGCTACTGA	TTCGTCTGCG	AGAACGTGGC	AACAGAGTTC	2640
TGATTTCTC	TCAGATGGTG	AGGATGCTGG	ACATCCTAGC	AGAATATCTG	AA GTATCGCC	2700
AGTTTCCCTT	CCAGAGACTT	GATGGATCAA	TAAAAGGGGA	ATTGAGGAAG	CAAGCACTGG	2760
ATCATTCAA	TGCAGAAGGA	TCAGAGGATT	TCTGTTTTT	ACTGTCTACA	AGAGCTGGAG	2820
GATTAGGTAT	TAACTTGGCA	TCTGCTGACA	CTGTAGTTAT	TTTGATTCT	GA CTGGAATC	2880
CACAGAATGA	TCTGCAGGCA	CAGGCGAGAG	CTCATAGAAT	TGGACAGAAAG	AAACAGGTTA	2940
ATATTTATCG	GCTAGTCACA	AAAGGATCAG	TAGAAGAAGA	TATTCTGAA	AGAGCCAAGA	3000
AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA	AAA ACTGTT	3060
TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTAA	TAAAGAAGAG	TTATCAGCTA	3120
TTTGAAAGTT	TGGTGCTGAG	GAACTCTTA	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	3180
AGGAAATGGA	TATAGATGAA	ATCTTGAAGA	GAGCTGAAAC	TCGGGAAAAT	GAGCCAGGTC	3240

CATTGACTGT AGGGGATGAG TTGCTTCAC AGTCAAGGT GGCGAACTT TCCAATATGG 3300
ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGAA GAAATCATCC 3360
CAGAATCCC ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT 3420
ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA 3480
GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC 3540
GCCAAAAAAA CGCTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTAGTG 3600
ATGCAGAGAT CAGGCCGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT 3660
TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC TGAGACAGAC CTTAGACGTT 3720
TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG 3780
AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCAAC GTTTCGAATC TCAGGAGTGC 3840
AGGTGAATGC AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACGT CACAATCCA 3900
TTCCTTCAGA TCCAGAAGAA AGGAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC 3960
ACTTCGATAT AGATTGGGT AAAGAAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT 4020
ATGGCTATGG CAGCTGGAA ATGATAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA 4080
TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT 4140
ACCTCATTAA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG 4200
CAGGCAATTG CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG GCTTCAAAAA 4260
TAAAAGAAGA AATAAAAGAGT GATTCTTCAC CACAACCCTC AGAAAAATCT GATGAAGATG 4320
ATGAGGAGGA GGATAACAAG GTAAATGAAA TGAAATCTGA AAATAAAGAA AAATCTAAA 4380
AAATTCCATT GCTGGATACT CCAGTTCATTA TTACTGCAAC CAGTGAACCA GTTCCTATCT 4440
CAGAAGAACATC TGAAGAACCT CATCAGAAGA CATTAGTGT GTGCAAAGAA AGAATGAGGC 4500
CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTCT GAAAGGGAGC 4560
AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGA TCACATTACA GAATGCCTGA 4620
AGGAGTACAC AAATCCCGAG CAAATAAAC AGTGGAGGAA AAATTGTGG ATTTTGTGT 4680
CCAAGTTAC AGAATTGAT GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAAA 4740
AGCGCCAAGA GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG 4800
TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT GATAGTAGCA 4860
GGGACAGTTA TTCTTCTGAT AGACATTAT CACAATACCA TGATCATCAC AAAGACAGGC 4920

ATCAGGGAGA TGCTTACAAG AAAAGTGACT CCAGGAAAAG GCCATATTCA GCCTTCAGTA	4980
ATGGAAAAGA TCACAGAGAC TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA	5040
GTAAACATAG AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA	5100
ACTTAAAAGA CAGCCGGGGT CATTCACTGC ACCGCTCCC TTCAGACCAC AGGATACACT	5160
CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC TTGAGAGAT TATAGATACC	5220
ACTCAGACTG GCAAATGGAC CACAGAGCTT CTGGTAGTGG CCCGAGGTCA CCACTAGATC	5280
AGAGGTCTCC TTATGGTTCA AGATCTCCCC TAGGACACAG ATCTCCATTG GAACACTCAT	5340
CAGATCACAA AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA	5400
CATTTCTGG ACCTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT TGCCTTACAT	5460
GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT ATTGTTACTT CTTTCCAGGA	5520
TGCAAGGTCT ATTATCCCAA CAGAAGAAAA ATATTTTGT ATTTAAAGTT TATGCTGCAC	5580
TGTGCTGCAA ATGTTGTGGC ACTTTTTTT TAAGAAATGG AAGATGTTA CTTTACAGG	5640
GACCTCAACA CTGCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG	5700
TTCTAGGCTG AACACAGATT AAATTATGTT TGAAATGAA CACTTAAACA CTGACCTGTG	5760
CTTATGTTTC AGGAAAGAAT GGGGGATTTA TTTGTTTA TTTCTGGTA GAGAACTCTC	5820
AAGGACTTTG TTCACCTTCC AAAGCTACTT GTTACATTG TACACTGCGA CCACCTGCC	5880
GCTTTCATC ACAAGCTTGA ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA	5940
TTTCTCCTGT TTGTGATCAG TTATAATGCC TTTTATGAA ACAAAACAAAC AAACAAAAAA	6000
CAATTAAAAA AAAAACACA ACAAAACAA CAAATGGCTG TAAATTATTG TAAATTAAATT	6060
AAATGAGCTT TTTCCGTCA GGCTTTTT GGCTGTTCT TTCCCCAACAA ACTCAGGCCT	6120
TCTTTCACA AAGTCAGTAT ACTTACATGT TTTAATAAAA TATCTCGATG GAATCAGAAT	6180
GTAAAAATGG GGAAGGGAAT ATTTTATTCC ATTTAGTGCT CCTTTTTAT TGGATACTTT	6240
TACATACCTG TTTTGGTTG TTTTATTTA TTTTTTTT CTATTAAACT GTCAGTGTG	6300
TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAC TGTGCCCTGG AAAGCTTTTC	6360
AGGTGCATTG GTTAAAGA AGGAAGTGTT CTATAGGTGA ACACCTCAAA ACCCAGATCA	6420
GCCAAGATTC ATTGTAAATC CATTGTTT CCCTCTTAA CATGGCAAT AATGTCAAAT	6480
GTGCTATGCA GCAGTTAATA TTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC	6540
AATGCACACT GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA	6600
AAAAAAACC	6608

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Glu Ile Val Ser Val Lys His Leu His Lys Lys Ile Lys Thr Glu
1 5 10 15

Lys Glu Asn Glu Glu Lys Pro Glu Pro Asp Ile Gly Ile Lys Lys Glu
20 25 30

Ala Glu Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys Arg Glu Leu
35 40 45

Lys Arg Glu Lys Lys Glu Lys Glu Asp Lys Lys Glu Leu Lys Glu Lys
50 55 60

Asp Asn Lys Glu Lys Arg Glu Asn Lys Val Lys Glu Ser Thr Gln Lys
65 70 75 80

Glu Lys Glu Val Lys Glu Glu Lys
85

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATGAGATTG TTTCA GTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA 60
AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA 120
AGAGAAGGAA ATA AAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAAGAGG ATAAGAAAAGA 180
ATTAAAAGAA AAAGATAATA AAGAAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA 240

AGAAAAAAGAA GTGAAGGAAG AGAAG

265

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATGGGATTG TTTCACTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA	60
AGAAAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA	120
AGAAAAGGAA ATAAGA	137

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu			
1	5	10	15
Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu			
20	25	30	
Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys			
35	40	45	

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA	60
AAGATGGTGT TAGATCATT AGTGATTCAAG AGAATGGACA CCACAGGGAA AACTGTACTA	120
CATACAGGCT CTACTCCTTC AAGCTCAACA CCTTTAATA AGGAAGAGTT ATCAGCAATT	180
TTGAAGTTG GTGCTGAGGA ACTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG	240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCA	300
TTAACTGTAG GAGATGAGTT ACTTTCACAG TTCAAGGTAG CTAACTTTC CAATATGGAT	360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGGAAGA AATCATTCCA	420
GAAGTTCACTGGT GGCGACGAAT AGAGGGGNNG GAAAGACAAA AAGAACTTGA AGAAATATAT	480
ATGCTTCAA GAATGAGAAA CTGTGAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA	540
TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA	600
CCAAAAAAAC GTGGACGACC ACGAACATT ATTCCCGTAAA ACATTAAGG ATTTAGTGAT	660
GCAGAGATTA GACGATTAT CAAGAGTTAC AAGAAATTG GTGGCCCAGT TGAAAGGTTA	720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG	780
GGAGAACTTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA	840
AGAACAGGTG GTAGATTG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG	900
GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT	960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCATT ACCACACCAA AGCAGCTCAT	1020
TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT	1080
GGTTATGGCA GTTGGAAAT GATAAAATG GATCCTGATC TCAGTTGAC ACAGAAGATT	1140
TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC	1200
CTCATTAAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA	1260
GGCAATTCAA AGAGGAGAAA AACAAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC	1316

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala
1 5 10 15

Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile
20 25 30

Leu Asp Leu His Leu Val Thr Val Asp Phe Leu Phe Asn Phe Leu Ile
35 40 45

Leu Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn Ser Ser
50 55 60

Gly Glu Ser Ser Arg Ser Asp Asp Asp Ser Ala Gly Ser Ala Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser Ser
85 90 95

Gln Ser Gly Ser Ser Asp Ser Glu Ser Gly Ser Glu Ser Gly Ser Gln
100 105 110

Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Lys Lys Gln Val Gln Ala
115 120 125

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser
130 135 140

Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln Gln
145 150 155 160

Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser
165 170 175

Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys
180 185 190

His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly
195 200 205

Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys
210 215 220

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
225 230 235 240

Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
245 250 255

Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Asp Asp Asp
260 265 270

Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
275 280 285

Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
290 295 300

Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
305 310 315 320

Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
325 330 335

Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
340 345 350

Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
355 360 365

Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
370 375 380

Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
385 390 395 400

Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
405 410 415

Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu
420 425 430

His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln
435 440 445

Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
450 455 460

Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys
465 470 475 480

Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
485 490 495

Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
500 505 510

Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu
515 520 525

Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
530 535 540

Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
545 550 555 560

Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
565 570 575

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser
580 585 590

Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val
595 600 605

Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp
610 615 620

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
625 630 635 640

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
645 650 655

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
660 665 670

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
675 680 685

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
690 695 700

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
705 710 715 720

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
725 730 735

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
740 745 750

Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
755 760 765

Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
770 775 780

Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
785 790 795 800

Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
805 810 815

Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile
820 825 830

Arg Ser Ser Gly Lys Leu Ile Leu Asp Lys Leu Leu Ile Arg Leu
835 840 845

Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
850 855 860

Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
865 870 875 880

Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
885 890 895

His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
900 905 910

Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
915 920 925

Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
930 935 940

Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
945 950 955 960

Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
965 970 975

Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
980 985 990

Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe
995 1000 1005

Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
1010 1015 1020

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
1025 1030 1035 1040

Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro
1045 1050 1055

Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
1060 1065 1070

Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
1075 1080 1085

Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu
1090 1095 1100

Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
1105 1110 1115 1120

Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
1125 1130 1135

Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser
1140 1145 1150

Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
1155 1160 1165

Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
1170 1175 1180

Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala
 1185 1190 1195 1200
 Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
 1205 1210 1215
 Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser
 1220 1225 1230
 Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro
 1235 1240 1245
 Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala.
 1250 1255 1260
 His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro
 1265 1270 1275 1280
 Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His
 1285 1290 1295
 Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly
 1300 1305 1310
 Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro
 1315 1320 1325
 Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys
 1330 1335 1340
 Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu
 1345 1350 1355 1360
 Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala
 1365 1370 1375
 Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met
 1380 1385 1390
 Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu
 1395 1400 1405
 Pro Ser Glu Lys Ser Asp Glu Asp Asp Lys Leu Asn Asp Ser Lys
 1410 1415 1420
 Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro
 1425 1430 1435 1440
 Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser
 1445 1450 1455
 Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg
 1460 1465 1470
 Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu
 1475 1480 1485

Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile
1490 1495 1500

Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln
1505 1510 1515 1520

Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr
1525 1530 1535

Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys
1540 1545 1550

Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala
1555 1560 1565

Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn
1570 1575 1580

Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His
1585 1590 1595 1600

Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser
1605 1610 1615

Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn
1620 1625 1630

Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr
1635 1640 1645

Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg
1650 1655 1660

Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg
1665 1670 1675 1680

Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg
1685 1690 1695

Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu
1700 1705 1710

Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu
1715 1720 1725

Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Ser
1730 1735 1740

Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe
1745 1750 1755 1760

Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu
1765 1770 1775

Arg Asn Gly Arg Cys Leu Leu Leu Gln Gly Pro Gln His Cys Pro Phe
1780 1785 1790

Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Val Val Leu Gly
1795 1800 1805

Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr
1810 1815 1820

Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe
1825 1830 1835 1840

Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys
1845 1850 1855

Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa
1860 1865 1870

Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro
1875 1880 1885

Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln
1890 1895 1900

Lys Thr Ile Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys
1905 1910 1915 1920

Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp
1925 1930 1935

Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr
1940 1945 1950

Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn
1955 1960 1965

Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Phe Tyr Trp Ile
1970 1975 1980

Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Phe Tyr
1985 1990 1995 2000

Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro
2005 2010 2015

Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg
2020 2025 2030

Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp
2035 2040 2045

Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val
2050 2055 2060

Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu
2065 2070 2075 2080

Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu
2085 2090 2095

Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr
2100 2105

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1795 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe Ala Leu Cys Pro Pro Val Thr Gln Arg Glu Pro Gln Glu Thr Arg
1 5 10 15

Glu Cys Arg Lys Phe Ile Phe Glu Ile Leu Ile Phe Glu Glu Ile Cys
20 25 30

Ile His Thr His Leu Leu Leu Ile Gly Asp Phe Cys Phe Ile Asn Phe
35 40 45

Leu Ile Phe Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn
50 55 60

Gly Ser Gly Glu Ser Ser Gln Ser Gly Asp Asp Cys Gly Ser Ala Ser
65 70 75 80

Gly Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser
85 90 95

Ser Gln Ser Gly Ser Ser Asp Ser Asp Ser Gly Ser Asp Ser Gly Ser
100 105 110

Gln Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala
115 120 125

Lys Pro Pro Lys Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser
130 135 140

Ile Leu Ala Val Gln Arg Ser Ala Met Leu Arg Lys Gln Pro Gln Gln
145 150 155 160

Ala Gln Gln Gln Arg Pro Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp
165 170 175

Ser Ser Ser Ser Glu Asp Ser Asp Asp Ser Ser Ser Gly Ala Lys Arg
180 185 190

Lys Lys His Asn Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro
195 200 205

Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser
210 215 220

Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg
225 230 235 240

Ser Arg Lys Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile
245 250 255

Leu Gly Gln Lys Lys Arg Gln Ile Asp Ser Ser Glu Asp Glu Asp Asp
260 265 270

Glu Asp Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val
275 280 285

Asn Val Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp
290 295 300

Leu Leu Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Asp Glu Glu
305 310 315 320

Phe Glu Thr Ile Glu Arg Val Met Asp Cys Arg Val Gly Arg Lys Gly
325 330 335

Ala Thr Gly Ala Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp
340 345 350

Pro Asn Ala Gly Phe Glu Arg Asn Lys Glu Pro Gly Asp Ile Gln Tyr
355 360 365

Leu Ile Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr
370 375 380

Glu Glu Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp
385 390 395 400

Asn Tyr Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala
405 410 415

Ser Pro Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp
420 425 430

Asp Leu His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser
435 440 445

Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln
450 455 460

Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser
465 470 475 480

Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser
485 490 495

Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg
500 505 510

Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly
515 520 525

Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His
530 535 540

Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu
545 550 555 560

Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu
565 570 575

His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu
580 585 590

Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala
595 600 605

Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His
610 615 620

Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu
625 630 635 640

Thr Thr Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu
645 650 655

Asn Trp Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp
660 665 670

Asp Ser Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg
675 680 685

Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp
690 695 700

Ser Leu Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp
705 710 715 720

Phe Glu Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu
725 730 735

His Lys Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val
740 745 750

Glu Lys Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met
755 760 765

Ser Ala Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr
770 775 780

Lys Ala Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn
785 790 795 800

Ile Met Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys
805 810 815

Pro Pro Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His
 820 825 830

 Leu Ile Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile
 835 840 845

 Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val
 850 855 860

 Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro
 865 870 875 880

 Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala
 885 890 895

 Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu
 900 905 910

 Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr
 915 920 925

 Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala
 930 935 940

 Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr
 945 950 955 960

 Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala
 965 970 975

 Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr
 980 985 990

 Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr
 995 1000 1005

 Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu
 1010 1015 1020

 Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met
 1025 1030 1035 1040

 Asp Ile Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro
 1045 1050 1055

 Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala
 1060 1065 1070

 Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg
 1075 1080 1085

 Asn Ser Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg
 1090 1095 1100

 Ile Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu
 1105 1110 1115 1120

Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu
1125 1130 1135

Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser
1140 1145 1150

Ile Thr Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile
1155 1160 1165

Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe
1170 1175 1180

Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala
1185 1190 1195 1200

Val Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg
1205 1210 1215

Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp
1220 1225 1230

Asn Ser Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys
1235 1240 1245

Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val
1250 1255 1260

Ile Ser His Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser
1265 1270 1275 1280

Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala
1285 1290 1295

Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu
1300 1305 1310

Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met
1315 1320 1325

Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp
1330 1335 1340

Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile
1345 1350 1355 1360

Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala
1365 1370 1375

Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys
1380 1385 1390

Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro
1395 1400 1405

Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Asp Asn Lys
1410 1415 1420

Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro
1425 1430 1435 1440

Leu Leu Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro
1445 1450 1455

Ile Ser Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys
1460 1465 1470

Lys Glu Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg
1475 1480 1485

Pro Glu Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln
1490 1495 1500

Cys Leu Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr
1505 1510 1515 1520

Thr Asn Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe
1525 1530 1535

Val Ser Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr
1540 1545 1550

Lys His Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln His Asn Asp Gln
1555 1560 1565

Asn Ile Ser Ser Asn Val Asn Thr His Val Ile Arg Asn Pro Asp Val
1570 1575 1580

Glu Arg Leu Lys Glu Thr Thr Asn His Asp Asp Ser Ser Arg Asp Ser
1585 1590 1595 1600

Tyr Ser Ser Asp Arg His Leu Ser Gln Tyr His Asp His His Lys Asp
1605 1610 1615

Arg His Gln Gly Asp Ala Tyr Lys Ser Asp Ser Arg Lys Arg Pro
1620 1625 1630

Tyr Ser Ala Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr
1635 1640 1645

Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp
1650 1655 1660

Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys
1665 1670 1675 1680

Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile
1685 1690 1695

His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser
1700 1705 1710

Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser
1715 1720 1725

Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser
1730 1735 1740

Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His
1745 1750 1755 1760

Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg
1765 1770 1775

Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His
1780 1785 1790

Ser Asn Cys
1795

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys Thr Xaa Glu Pro Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly
1 5 10 15

Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln
20 25 30

Gln Asn Val Arg Gly Met Lys Lys Leu Asp Asn Tyr Lys Lys Lys Asp
35 40 45

Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro Glu Asp Val Glu
50 55 60

Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu His Lys Gln Tyr
65 70 75 80

Gln Ile Val Glu Arg Thr Asn Xaa Ser Phe Gln Ser Lys Ser Ala Ala
85 90 95

Gly Tyr Pro

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile Tyr Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu
1 5 10 15

Arg Ala Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met
20 25 30

Asp Thr Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser
35 40 45

Ser Thr Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly
50 55 60

Ala Glu Glu Leu Phe Lys Glu Pro Glu Xaa Glu Glu Glu Pro Gln
65 70 75 80

Glu Met Asp Ile Asp Glu Ile Leu Lys Arg Xaa Glu Thr Arg Glu Asn
85 90 95

Glu Ser Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys
100 105 110

Val Ala Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro
115 120 125

Glu Gln Asn Leu Arg Asn Trp Glu Glu Ile Ile Pro Glu Val Gln Trp
130 135 140

Arg Arg Ile Glu Gly Xaa Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr
145 150 155 160

Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly
165 170 175

Asn Glu Gly Arg Cys Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser
180 185 190

Asp Ser Ile Ser Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg
195 200 205

Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg
210 215 220

Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Val Glu Arg Leu
225 230 235 240

Asp Ala Ile Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp
245 250 255

Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu
260 265 270

Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys
275 280 285

Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys
290 295 300

Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile
305 310 315 320

Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr
325 330 335

Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn
340 345 350

Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile
355 360 365

Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp
370 375 380

Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr
385 390 395 400

Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg
405 410 415

Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys
420 425 430

Asn Lys Ala Thr Lys Ala Ala
435

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1434
- (D) OTHER INFORMATION:/note= "The sequence beginning at 1 corresponds to 55 and that ending at 1434 corresponds to 1488"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser
1 5 10 15

Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln
20 25 30

Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser
35 40 45

Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys
50 55 60

His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly
65 70 75 80

Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys
85 90 95

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
100 105 110

Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Ser Thr Gly
115 120 125

Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Asp Asp Asp
130 135 140

Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
145 150 155 160

Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
165 170 175

Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
180 185 190

Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
195 200 205

Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
210 215 220

Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
225 230 235 240

Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
245 250 255

Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
260 265 270

Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
275 280 285

Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu
290 295 300

His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln
305 310 315 320

Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
325 330 335

Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys
340 345 350

Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
355 360 365

Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
370 375 380

Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu
385 390 395 400

Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
405 410 415

Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
420 425 430

Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
435 440 445

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser
450 455 460

Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val
465 470 475 480

Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp
485 490 495

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
500 505 510

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
515 520 525

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
530 535 540

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
545 550 555 560

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
565 570 575

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
580 585 590

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
595 600 605

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
610 615 620

Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
625 630 635 640

Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
645 650 655

Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
660 665 670

Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
675 680 685

Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile
690 695 700

Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu
705 710 715 720

Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
725 730 735

Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
740 745 750

Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
755 760 765

His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
770 775 780

Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
785 790 795 800

Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
805 810 815

Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
820 825 830

Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
835 840 845

Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
850 855 860

Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr Pro Phe
865 870 875 880

Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
885 890 895

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
900 905 910

Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro Gly Pro
915 920 925

Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
930 935 940

Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
945 950 955 960

Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg Ile Glu
965 970 975

Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
980 985 990

Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
995 1000 1005

Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Thr
1010 1015 1020

Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
1025 1030 1035 1040

Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
1045 1050 1055

Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala
1060 1065 1070

Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
1075 1080 1085

Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser
1090 1095 1100

Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro
1105 1110 1115 1120

Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser
1125 1130 1135

His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro
1140 1145 1150

Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His
1155 1160 1165

Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly
1170 1175 1180

Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro
1185 1190 1195 1200

Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys
1205 1210 1215

Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu
 1220 1225 1230

Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala Gly Ala
 1235 1240 1245

Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys Met Lys
 1250 1255 1260

Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Gln Pro
 1265 1270 1275 1280

Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Asp Asn Lys Val Asn
 1285 1290 1295

Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro Leu Leu
 1300 1305 1310

Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro Ile Ser
 1315 1320 1325

Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys Lys Glu
 1330 1335 1340

Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu
 1345 1350 1355 1360

Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu
 1365 1370 1375

Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Thr Asn
 1380 1385 1390

Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser
 1395 1400 1405

Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His
 1410 1415 1420

Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln
 1425 1430

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1467 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..1467
 - (D) OTHER INFORMATION:/note= "The sequence beginning at 1

corresponds to 2654 and that ending at 1467 corresponds to
4120"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Ala Ala Lys Asp Ile Ser Thr Glu Val Leu Gln Asn Pro Glu Leu
1 5 10 15

Tyr Gly Leu Arg Arg Ser His Arg Ala Ala Ala His Gln Gln Asn Tyr
20 25 30

Phe Asn Asp Ser Asp Asp Glu Asp Asp Glu Asn Ile Lys Gln Ser
35 40 45

Arg Arg Lys Arg Met Thr Thr Ile Glu Asp Asp Glu Asp Glu Phe Glu
50 55 60

Asp Glu Glu Gly Glu Glu Asp Ser Gly Glu Asp Glu Asp Glu Asp
65 70 75 80

Phe Glu Glu Asp Asp Asp Tyr Tyr Gly Ser Pro Ile Lys Gln Asn Arg
85 90 95

Ser Lys Pro Lys Ser Arg Thr Lys Ser Lys Ser Lys Pro Lys
100 105 110

Ser Gln Ser Glu Lys Gln Ser Thr Val Lys Ile Pro Thr Arg Phe Ser
115 120 125

Asn Arg Gln Asn Lys Thr Val Asn Tyr Asn Ile Asp Tyr Ser Asp Asp
130 135 140

Asp Leu Leu Glu Ser Glu Asp Asp Tyr Gly Ser Glu Glu Ala Leu Ser
145 150 155 160

Glu Glu Asn Val His Glu Ala Ser Ala Asn Pro Gln Pro Glu Asp Phe
165 170 175

His Gly Ile Asp Ile Val Ile Asn His Arg Leu Lys Thr Ser Leu Glu
180 185 190

Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys
195 200 205

Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His
210 215 220

Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys
225 230 235 240

Arg Leu Asp Asn Tyr Cys Lys Gln Phe Ile Ile Glu Asp Gln Gln Val
245 250 255

Arg Leu Asp Pro Tyr Val Thr Ala Glu Asp Ile Glu Ile Met Asp Met
260 265 270

Glu Arg Glu Arg Arg Leu Asp Glu Phe Glu Glu Phe His Val Pro Glu
275 280 285

Arg Ile Ile Asp Ser Gln Arg Ala Ser Leu Glu Asp Gly Thr Ser Gln
290 295 300

Leu Gln Tyr Leu Val Lys Trp Arg Arg Leu Asn Tyr Asp Glu Ala Thr
305 310 315 320

Trp Glu Asn Ala Thr Asp Ile Val Lys Leu Ala Pro Glu Gln Val Lys
325 330 335

His Phe Gln Asn Arg Glu Asn Ser Lys Ile Leu Pro Gln Tyr Ser Ser
340 345 350

Asn Tyr Thr Ser Gln Arg Pro Arg Phe Glu Lys Leu Ser Val Gln Pro
355 360 365

Pro Phe Ile Lys Gly Gly Glu Leu Arg Asp Phe Gln Leu Thr Gly Ile
370 375 380

Asn Trp Met Ala Phe Leu Trp Ser Lys Gly Asp Asn Gly Ile Leu Ala
385 390 395 400

Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Val Ala Phe Ile Ser
405 410 415

Trp Leu Ile Phe Ala Arg Arg Gln Asn Gly Pro His Ile Ile Val Val
420 425 430

Pro Leu Ser Thr Met Pro Ala Trp Leu Asp Thr Phe Glu Lys Trp Ala
435 440 445

Pro Asp Leu Asn Cys Ile Cys Tyr Met Gly Asn Gln Lys Ser Arg Asp
450 455 460

Thr Ile Arg Glu Tyr Glu Phe Tyr Thr Asn Pro Arg Ala Lys Gly Lys
465 470 475 480

Lys Thr Met Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Leu
485 490 495

Lys Asp Arg Ala Glu Leu Gly Ser Ile Lys Trp Gln Phe Met Ala Val
500 505 510

Asp Glu Ala His Arg Leu Lys Asn Ala Glu Ser Ser Leu Tyr Glu Ser
515 520 525

Leu Asn Ser Phe Lys Val Ala Asn Arg Met Leu Ile Thr Gly Thr Pro
530 535 540

Leu Gln Asn Asn Ile Lys Glu Leu Ala Ala Leu Val Asn Phe Leu Met
545 550 555 560

Pro Gly Arg Phe Thr Ile Asp Gln Glu Ile Asp Phe Glu Asn Gln Asp
565 570 575

Glu Glu Gln Glu Glu Tyr Ile His Asp Leu His Arg Arg Ile Gln Pro
580 585 590

Phe Ile Leu Arg Arg Leu Lys Lys Asp Val Glu Lys Ser Leu Pro Ser
595 600 605

Lys Thr Glu Arg Ile Leu Arg Val Glu Leu Ser Asp Val Gln Thr Glu
610 615 620

Tyr Tyr Lys Asn Ile Leu Thr Lys Asn Tyr Ser Ala Leu Thr Ala Gly
625 630 635 640

Ala Lys Gly Gly His Phe Ser Leu Leu Asn Ile Met Asn Glu Leu Lys
645 650 655

Lys Ala Ser Asn His Pro Tyr Leu Phe Asp Asn Ala Glu Glu Arg Val
660 665 670

Leu Gln Lys Phe Gly Asp Gly Lys Met Thr Arg Glu Asn Val Leu Arg
675 680 685

Gly Leu Ile Met Ser Ser Gly Lys Met Val Leu Leu Asp Gln Leu Leu
690 695 700

Thr Arg Leu Lys Lys Asp Gly His Arg Val Leu Ile Phe Ser Gln Met
705 710 715 720

Val Arg Met Leu Asp Ile Leu Gly Asp Tyr Leu Ser Ile Lys Gly Ile
725 730 735

Asn Phe Gln Arg Leu Asp Gly Thr Val Pro Ser Ala Gln Arg Arg Ile
740 745 750

Ser Ile Asp His Phe Asn Ser Pro Asp Ser Asn Asp Phe Val Phe Leu
755 760 765

Leu Ser Thr Arg Ala Gly Leu Gly Ile Asn Leu Met Thr Ala Asp
770 775 780

Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Ala Asp Leu Gln
785 790 795 800

Ala Met Ala Arg Ala His Arg Ile Gly Gln Lys Asn His Val Met Val
805 810 815

Tyr Arg Leu Val Ser Lys Asp Thr Val Glu Glu Glu Val Leu Glu Arg
820 825 830

Ala Arg Lys Lys Met Ile Leu Glu Tyr Ala Ile Ile Ser Leu Gly Val
835 840 845

Thr Asp Gly Asn Lys Tyr Thr Lys Lys Asn Glu Pro Asn Ala Gly Glu
850 855 860

Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr
865 870 875 880

Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn
885 890 895

His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu
900 905 910

Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala
915 920 925

Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Glu Leu Lys Lys Leu
930 935 940

Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln
945 950 955 960

Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn
965 970 975

Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp
980 985 990

Ser Thr Ser Arg Ser Ser Arg Arg Arg Ala Arg Ala Asn Asp Met Asp
995 1000 1005

Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys
1010 1015 1020

Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr
1025 1030 1035 1040

Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met
1045 1050 1055

Met Glu Ala Ala Lys Asp Cys Val His Glu Glu Glu Lys Asn Arg Lys
1060 1065 1070

Glu Ile Leu Glu Lys Leu Glu Lys His Ala Thr Ala Tyr Arg Ala Lys
1075 1080 1085

Leu Lys Ser Gly Glu Ile Lys Ala Glu Asn Gln Pro Lys Asp Asn Pro
1090 1095 1100

Leu Thr Arg Leu Ser Leu Lys Lys Arg Glu Lys Lys Ala Val Leu Phe
1105 1110 1115 1120

Asn Phe Lys Gly Val Lys Ser Leu Asn Ala Glu Ser Leu Leu Ser Arg
1125 1130 1135

Val Glu Asp Leu Lys Tyr Leu Lys Asn Leu Ile Asn Ser Asn Tyr Lys
1140 1145 1150

Asp Asp Pro Leu Lys Phe Ser Leu Gly Asn Asn Thr Pro Lys Pro Val
1155 1160 1165

Gln Asn Trp Ser Ser Asn Trp Thr Lys Glu Glu Asp Glu Lys Leu Leu
1170 1175 1180

Ile Gly Val Phe Lys Tyr Gly Tyr Gly Ser Trp Thr Gln Ile Arg Asp
 1185 1190 1195 1200
 Asp Pro Phe Leu Gly Ile Thr Asp Lys Ile Phe Leu Asn Glu Val His
 1205 1210 1215
 Asn Pro Val Ala Lys Lys Ser Ala Ser Ser Ser Asp Thr Thr Pro Thr
 1220 1225 1230
 Pro Ser Lys Lys Gly Lys Gly Ile Thr Gly Ser Ser Lys Lys Val Pro
 1235 1240 1245
 Gly Ala Ile His Leu Gly Arg Arg Val Asp Tyr Leu Leu Ser Phe Leu
 1250 1255 1260
 Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys
 1265 1270 1275 1280
 Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn
 1285 1290 1295
 His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn
 1300 1305 1310
 Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala
 1315 1320 1325
 Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu
 1330 1335 1340
 Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro
 1345 1350 1355 1360
 Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu
 1365 1370 1375
 Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu
 1380 1385 1390
 Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu
 1395 1400 1405
 Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly
 1410 1415 1420
 Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser
 1425 1430 1435 1440
 Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met
 1445 1450 1455
 Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys
 1460 1465

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn	Ala	Gly	Phe	Glu	Lys	Ser	Lys
1				5					10				15		
Glu	Leu	Gly	Glu	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Trp	Ser	His
	20						25					30			
Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln	Gln	Asn	Val
	35					40					45				
Lys	Gly	Met	Asn	Lys	Leu	Asp	Asn	Tyr	Lys	Lys					
	50					55									

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn	Ala	Gly	Phe	Glu	Arg	Asn	Lys
1				5					10				15		
Glu	Pro	Gly	Asp	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Trp	Ser	His
	20						25					30			
Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln	Gln	Asn	Val
	35					40					45				
Arg	Gly	Asn	Lys	Lys	Leu	Asp	Asn	Tyr	Lys	Lys					
	50					55									

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys
1 5 10 15

Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His
20 25 30

Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys
35 40 45

Arg Leu Asp Asn Tyr Cys Lys
50 55

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu Glu Glu Glu Glu Tyr Ala Val Glu Lys Ile Ile Asp Arg Arg Val
1 5 10 15

Arg Lys Gly Lys Val Glu Tyr Tyr Leu Lys Trp Lys Gly Tyr Pro Glu
20 25 30

Thr Glu Asn Thr Trp Glu Pro Glu Asn Asn Leu Asp Cys Gln Asp Leu
35 40 45

Ile Gln Gln Tyr
50

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val
1 5 10 15

Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser
20 25 30

Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu
35 40 45

Leu Ile Ser Glu Phe
50

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val
1 5 10 15

Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp
20 25 30

Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu
35 40 45

Ile Ala Glu Phe
50

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val
1 5 10 15

Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp
20 25 30

Ala Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Glu Leu
35 40 45

Ile Glu Asp Phe
50

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro Val Asp Leu Val Tyr Ala Ala Glu Lys Ile Ile Gln Lys Arg Val
1 5 10 15

Lys Lys Gly Val Val Glu Tyr Arg Val Lys Trp Lys Gly Trp Asn Gln
20 25 30

Arg Tyr Asn Thr Trp Glu Pro Glu Asn Asn Ile Leu Asp Arg Arg Leu
35 40 45

Ile Asp Ile Tyr
50

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu
1 5 10 15

Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser
20 25 30

Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu
35 40 45

Leu Leu Ala Phe
50

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG 60
CGACCCCCGCA CTATCCCTCG GGAGAAATATT AAAGGATTAA GTGATGCCGA G 111

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGACTCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGGG 60
AGACCTCGAA CCATTCCTCG AGAAAATATT AAAGGATTAA GTGATGCCGA G 111

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCCAAAAAA GCGTGGAAAGA CCACGAACTA TTCCCTCGAGA	60
AAATATA	67

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAAA AAAACGTGGA	60
CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTAA GTGATGCAGA G	111

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAACTA TTCCCTCGTGA	60
AAATATT	67

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGACTCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA	60
CTATCCCTCG GGAGAATATT AAAGGATTAA GCGATGCAGA GATTAGGCAG T	111

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC	24
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(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA	23
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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Lys Arg Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Arg Gly Arg Pro Arg
1 5